

FIG 1

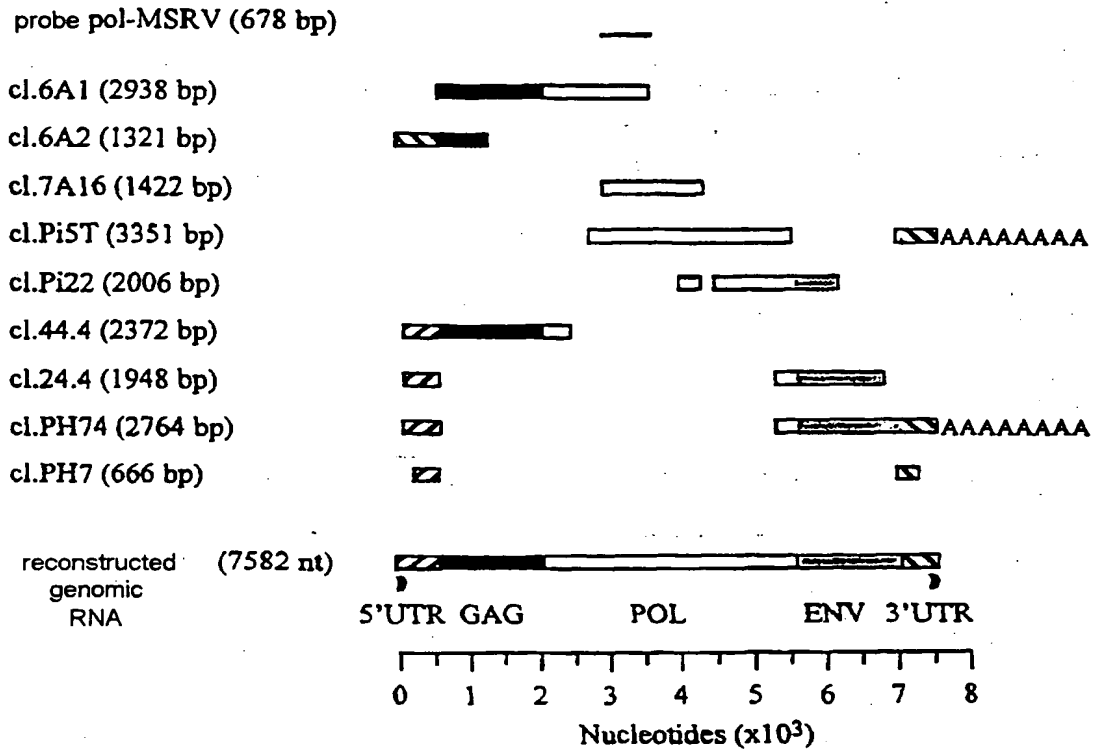
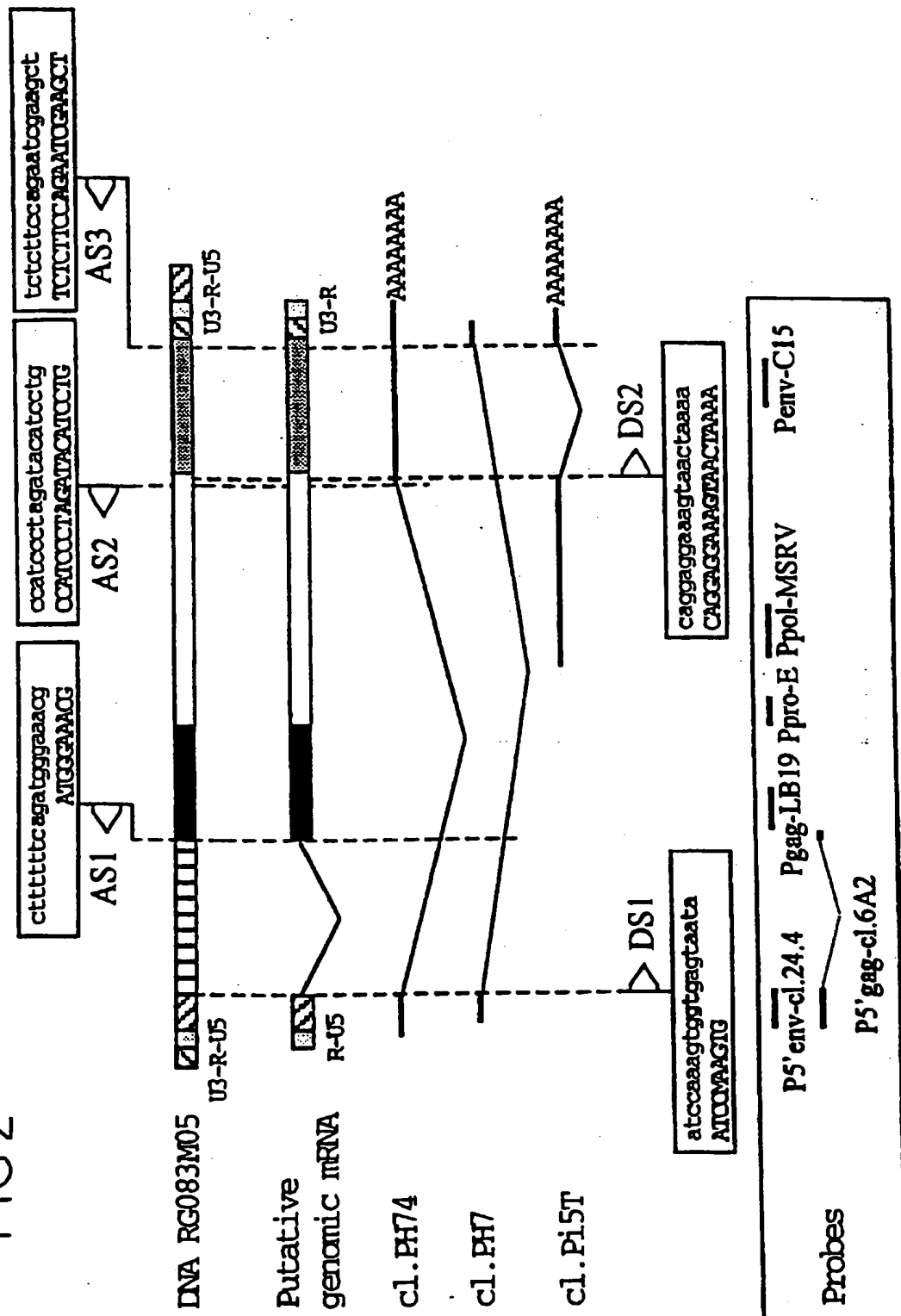


FIG 2



# FIG 3

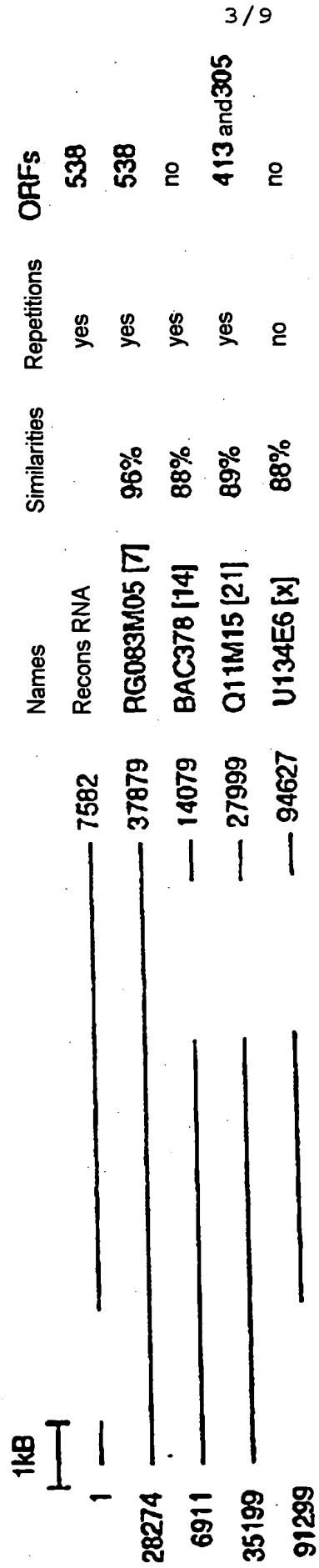


FIG 4A

LTR

0.02

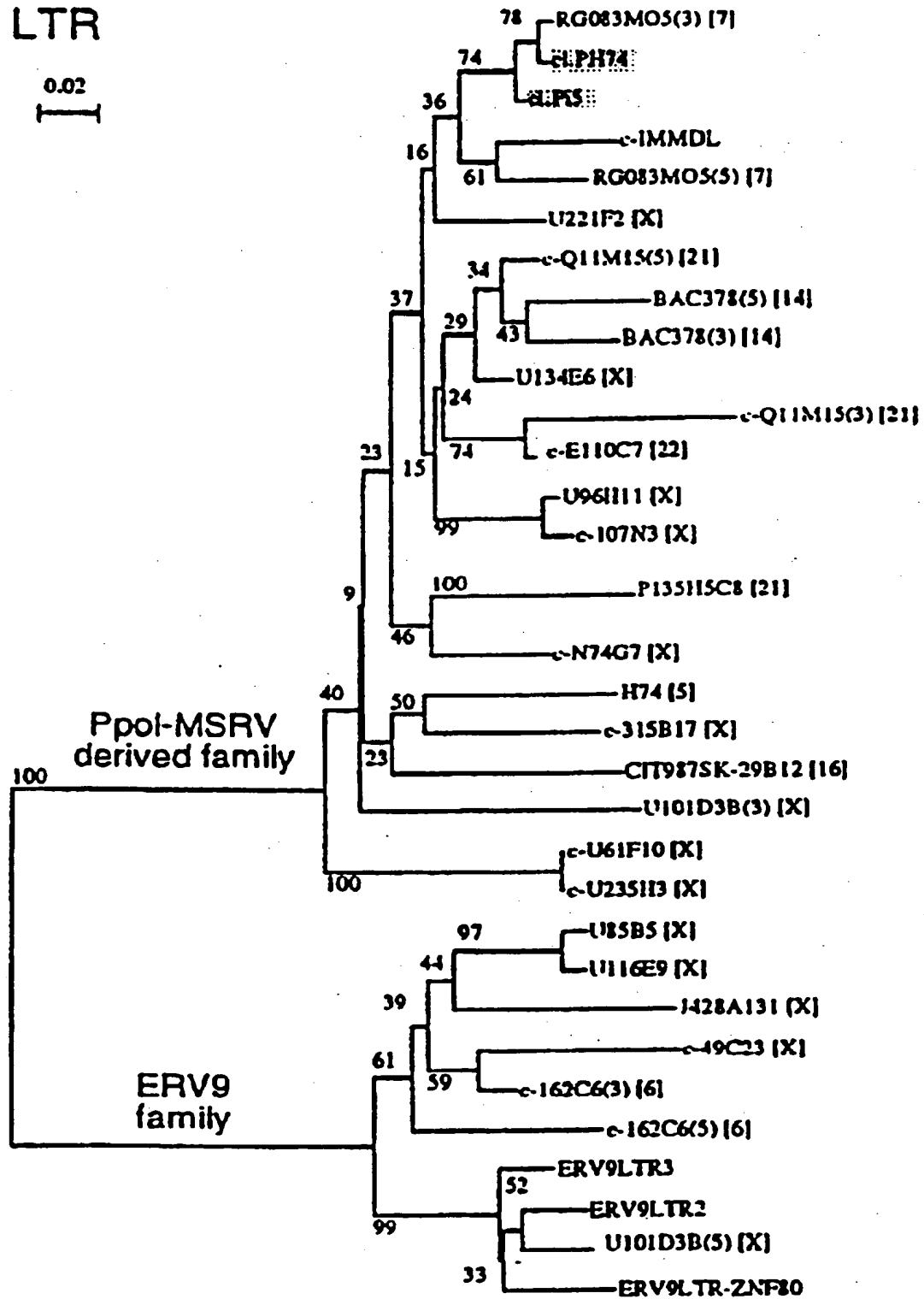


FIG 4 B

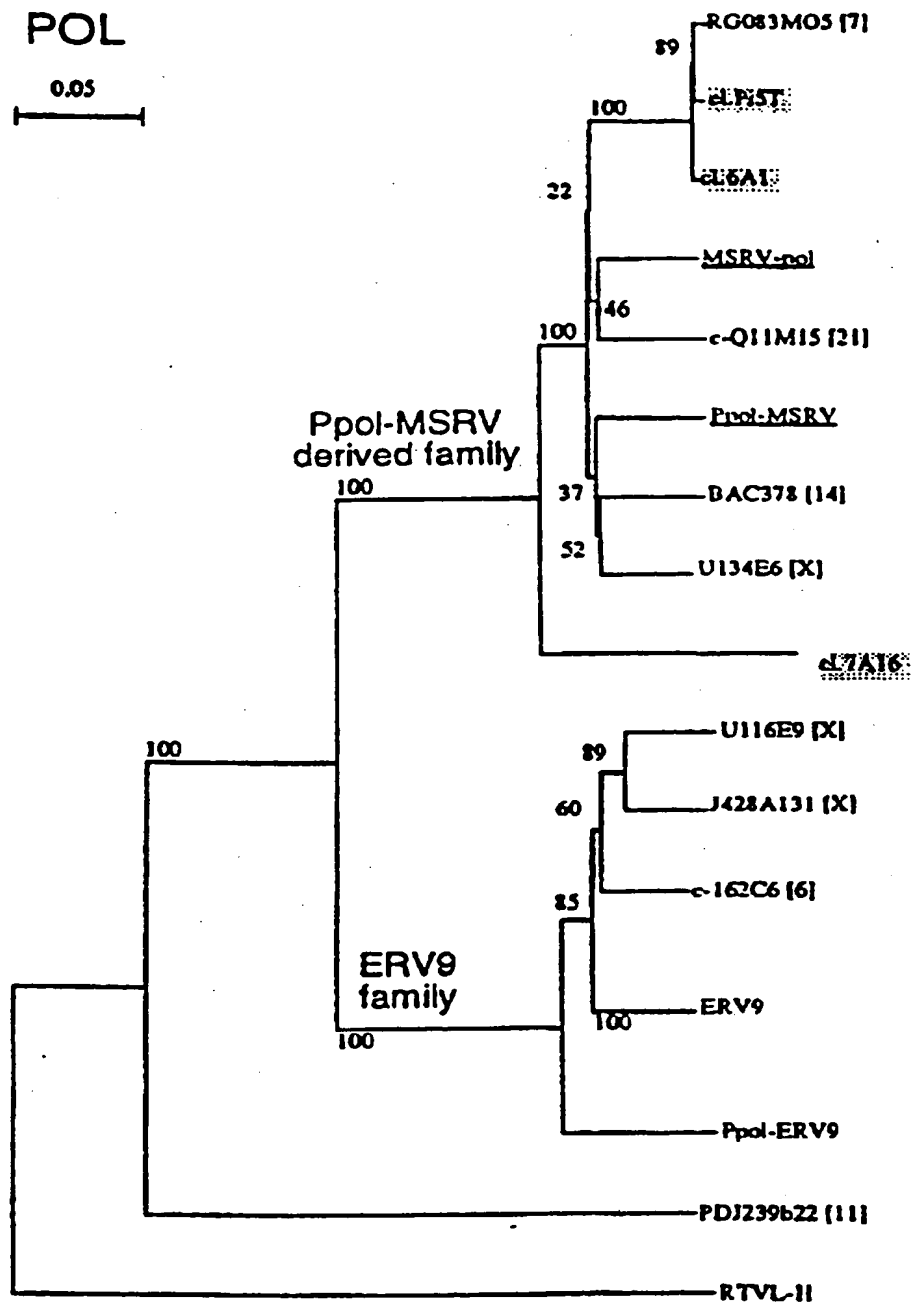
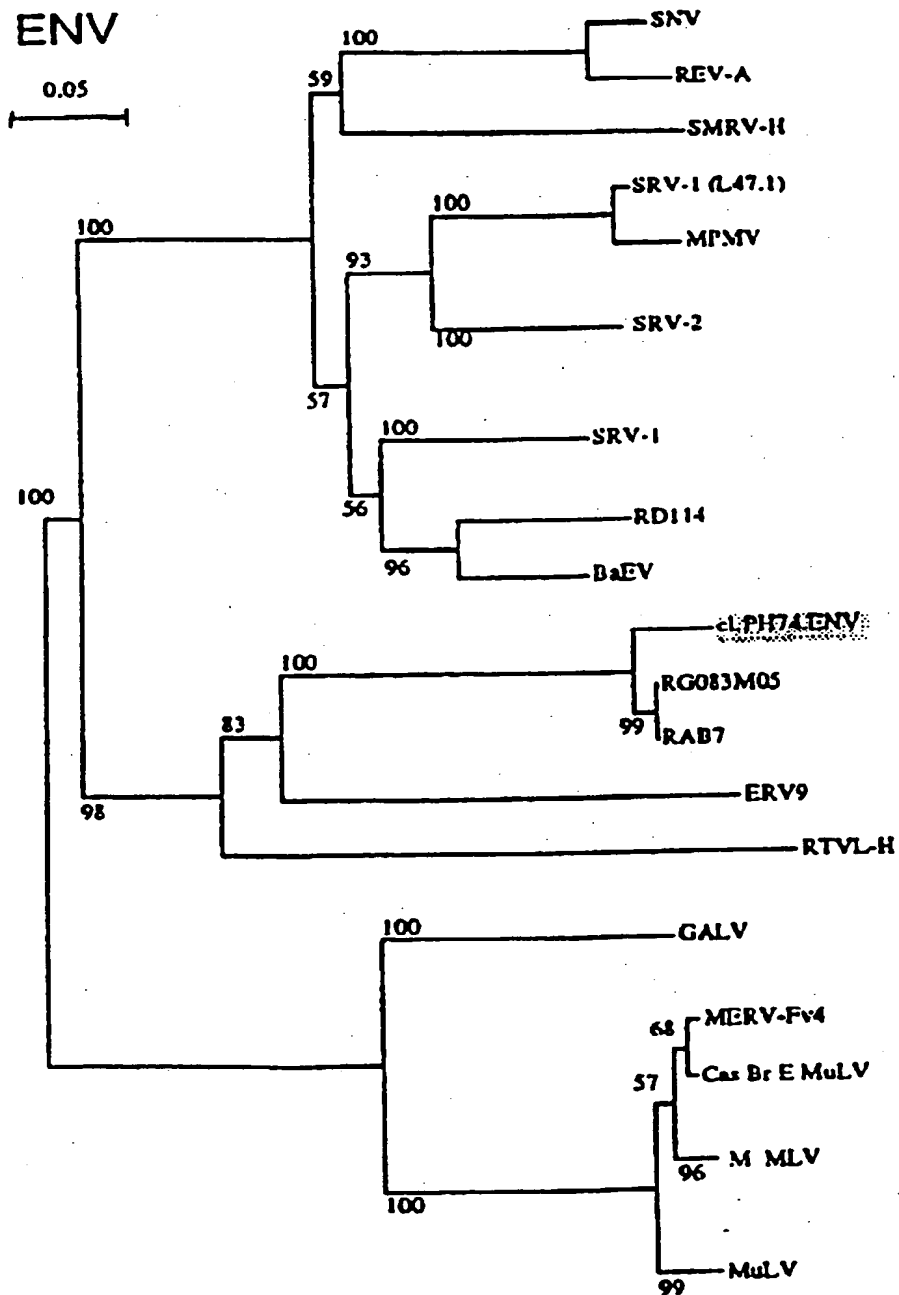


FIG 4C



## FIG 5A

[illegible]

FIG 5B

Accession	Sequence	Position
5-RG-28000-28872	CCGACGAGCTGCGCGCTGACCTCCATCCCTCTGGATCTCCAGGGGTGTCGGCTGCTCTGATCCACGAGGGGCGCCCATTTGCGGCTCCCAATTTGGGCTAAAGGCTTGGCCATTTGTTCTCTGC	572
3-RG-37500-38314	CCGACGAGCGCGCGCTGACCTCCATCCCTCTGGATCTCCAGGGGTGTCGGCTGCTCTGATCCACGAGGGGCGCCCATTTGCGGCTCCCAATTTGGGCTTGGCCATTTGTTCTCTGC	572
5-6A2.1-600	CCGACGAGCTGCGCGCTGACCTCCATCCCTCTGGATCTCCAGGGGTGTCGGCTGCTCTGATCCACGAGGGGCGCCCATTTGCGGCTCCCAATTTGGGCTTGGCCATTTGTTCTCTGC	312
5-PH74.1-530	CCGACGAGCTGCGCGCTGACCTCCATCCCTCTGGATCTCCAGGGGTGTCGGCTGCTCTGATCCACGAGGGGCGCCCATTTGCGGCTCCCAATTTGGGCTTGGCCATTTGTTCTCTGC	241
5-24.4.1-486	CCGACGAGCTGCGCGCTGACCTCCATCCCTCTGGATCTCCAGGGGTGTCGGCTGCTCTGATCCACGAGGGGCGCCCATTTGCGGCTCCCAATTTGGGCTTGGCCATTTGTTCTCTGC	198
Consensus	CCGACGAGCTGCGCGCTGACCTCCATCCCTCTGGATCTCCAGGGGTGTCGGCTGCTCTGATCCACGAGGGGCGCCCATTTGCGGCTCCCAATTTGGGCTTGGCCATTTGTTCTCTGC	520
5-RG-28000-28872	ACGGCTTAAGTGCCTGGGTTTGTCTTAATTGAGCTGAACACTAGCTACTGGGTTCCATGGGTTCTCTCTGTGTGACCCAGGGCTTCTTAATAGAACCTATTAACACTTAACACATGAGGCCGCCCAAGATT	705
3-RG-37500-38314	ATGGCTTAAGTGCCTGGGTTTGTCTTAATTGAGCTGAACACTAGCTACTGGGTTCCATGGGTTCTCTCTGTGTGACCCAGGGCTTCTTAATAGAACCTATTAACACTTAACACATGAGGCCGCCCAAGATT	692
5-6A2.1-600	ACGGCTTAAGTGCCTGGGTTTGTCTTAATTGAGCTGAACACTAGCTACTGGGTTCCATGGGTTCTCTCTGTGTGACCCAGGGCTTCTTAATAGAACCTATTAACACTTAACACATGAGGCCGCCCAAGATT	432
5-PH74.1-530	ACGGCTTAAGTGCCTGGGTTTGTCTTAATTGAGCTGAACACTAGCTACTGGGTTCCATGGGTTCTCTCTGTGTGACCCAGGGCTTCTTAATAGAACCTATTAACACTTAACACATGAGGCCGCCCAAGATT	361
5-24.4.1-486	ACGGCTTAAGTGCCTGGGTTTGTCTTAATTGAGCTGAACACTAGCTACTGGGTTCCATGGGTTCTCTCTGTGTGACCCAGGGCTTCTTAATAGAACCTATTAACACTTAACACATGAGGCCGCCCAAGATT	318
Consensus	ACGGCTTAAGTGCCTGGGTTTGTCTTAATTGAGCTGAACACTAGCTACTGGGTTCCATGGGTTCTCTCTGTGTGACCCAGGGCTTCTTAATAGAACCTATTAACACTTAACACATGAGGCCGCCCAAGATT	640
5-RG-28000-28872	CCATTCCTCTTGGAATCCGTGAGGCCAA-GAATCTCGGTGAGAGATACGAGGCTTGCACCACTCTCTGGAGCGGCTGCTACCACTCTTGGAGAGTGGTTTCACACCACTTCTTGGAGGCTCTG	824
3-RG-37500-38314	CCATTCCTCTTGGAATCCGTGAGGCCAA-GAATCTCGGTGAGAGATACGAGGCTTGCACCACTCTCTGGAGCGGCTGCTACCACTCTTGGAGAGTGGTTTCACACCACTTCTTGGAGGCTCTG	766
5-6A2.1-600	CCATTCCTCTTGGAATCCGTGAGGCCAA-GAATCTCGGTGAGAGATACGAGGCTTGCACCACTCTCTGGAGCGGCTGCTACCACTCTTGGAGAGTGGTTTCACACCACTTCTTGGAGGCTCTG	551
5-PH74.1-530	CCATTCCTCTTGGAATCCGTGAGGCCAA-GAATCTCGGTGAGAGATACGAGGCTTGCACCACTCTCTGGAGCGGCTGCTACCACTCTTGGAGAGTGGTTTCACACCACTTCTTGGAGGCTCTG	481
5-24.4.1-486	CCATTCCTCTTGGAATCCGTGAGGCCAA-GAATCTCGGTGAGAGATACGAGGCTTGCACCACTCTCTGGAGCGGCTGCTACCACTCTTGGAGAGTGGTTTCACACCACTTCTTGGAGGCTCTG	437
Consensus	CCATTCCTCTTGGAATCCGTGAGGCCAA-GAATCTCGGTGAGAGATACGAGGCTTGCACCACTCTCTGGAGCGGCTGCTACCACTCTTGGAGAGTGGTTTCACACCACTTCTTGGAGGCTCTG	760
5-RG-28000-28872	TGAGCAGAGGACCGCCCGGTACACATTTTGGCAACCAAGACCGGACATCCA	873
3-RG-37500-38314	TGAGCAGAGGACCGCCCGGTACACATTTTGGCAACCAAGACCGGACATCCA	815
5-6A2.1-600	TGAGCAGAGGACCGCCCGGTACACATTTTGGCAACCAAGACCGGACATCCA	600
5-PH74.1-530	TGAGCAGAGGACCGCCCGGTACACATTTTGGCAACCAAGACCGGACATCCA	530
5-24.4.1-486	TGAGCAGAGGACCGCCCGGTACACATTTTGGCAACCAAGACCGGACATCCA	486
Consensus	TGAGCAGAGGACCGCCCGGTACACATTTTGGCAACCAAGACCGGACATCCA	783



# ORF1: ENV (538 AA) FIG 6

```

<--- L ---><--- SU
MGLPYHIFLCVLSPCFTLTAPPPCRMTSSSPHPEFLWRMQRPGNIDAPSYRSLSKGTP 60
A FT V S YQ C

TFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCPGGLGVTVCWTYFTQTGMSDGGGV 120

QDQAREKHVKEVISOLTG VHGTS SPYKGLDLSKLHETLRTHTRLVSLFNTTLTGLHEVSA 180
R

QNPTNCWICLPLNFRPYVSI PVPEQWNNFSTEINTTSVLVGPLVSNVEITHTSNLTCVKF 240
L

SNTTYTTNSQCIRWVTPPTQIVCLPSGIFFVCGTSAYRCLNGSSESMCFLSFLVPPMAIY 300
T

-----><--- TM
TEQDLYSYVISKPRNKRVPILPFVIGAGVLGALGTGIGGITTSTQFYKLSQELNGDMER 360

VADSLVTLDQQLNSLA AVLQNRALDLLTAERGGTCLFLGEECCYYVNQSGIVTEKVEE 420
R S K

IPDRIQRIAEELRNTGPWGLLSRWMPWILPFLGPLAAIILLLLFGPCIFDLLVNFVSSRI 480
R R Q N

EAVKLQMEPKMQSKTKIYRRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS 538

```

## ORF2 (52AA)

MEPKMQSKTKIYRRPLDRPVSPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS-

Alignment ORF2 and Rex PLLV-L

```

ORF2          KIY-RRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRP
++Y          LD P SP ++          P S QPLLRP
Rex PTLV-L (B53482) RLYNTLSLDSPPSPKELPA-----PSRFSPQPLLRP

```

## ORF3 (48AA)

MLMTSKAPLLRKSQ LHNLYYAPIQQEAVRAVVGQPPQHLGFPVEMGD

Alignment ORF3 and Tat SIV-AGM

```

ORF3          MTSKAPLLRKSQ LHNLYYAPIQQEAVRAVVGQPPQ
+T AP R+ ++ +L AP+Q +++ G+ Q
Tat SIV-AGM(p05913) VTYHAPRTRRKKIRSLNLAPLQHQSISTKWGRDGO

```